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SEQUENCE LISTING

<110> J. Turck
 J. Archer
 <120> CONTROL OF GENE EXPRESSION IN EUKARYOTES
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Gln Arg Met Trp Asp Leu Ser Asp Phe Leu Ile Asn Thr Thr Gly Ile
180 185 190
Thr Asn Pro Leu Ser Ser Ala Leu Pro Asp Arg Gln His Asp His His
195 200 205
Glu Ile Thr Glu Ala Ile Arg Asn Arg Asp Ala Ala Ala Arg Glu
210 215 220
Ala Met Glu Arg His Ile Val Gly Thr Ile Ala Val Ile Arg Asp Glu
225 230 235
Ser Asn Ala Gln Leu Pro Ser
240 245

<210> 3

<211> 515

<212> PRT

<213> Rhodococcus sp.

<400> 3

Val Leu Pro Leu Glu Asp Ser Pro Glu Asn Pro Ser Arg Thr Ser
1 5 10 15
Pro Glu Glu Arg Ser Gly His Asp Asp Arg Phe Ala Arg Ile Val Leu
20 25 30
Arg Gly Thr Ser Pro Leu Pro Pro Thr Asp Arg Gly Ser Pro Thr Val
35 40 45
Ser Thr Thr Pro Thr Ser Pro Thr Lys Thr Ser Pro Leu Arg Val Ala
50 55 60

Met Ala Ser Phe Ile Gly Thr Thr Val Glu Tyr Tyr Asp Phe Phe Ile
 65 70 75
 Tyr Gly Thr Ala Ala Ala Leu Val Phe Pro Glu Leu Phe Phe Pro Asp
 80 85 90 95
 Val Ser Ser Ala Ile Gly Ile Leu Leu Ser Phe Ala Thr Phe Ser Val
 100 105 110
 Gly Phe Leu Ala Arg Pro Leu Gly Gly Ile Val Phe Gly His Phe Gly
 115 120 125
 Asp Arg Val Gly Arg Lys Gln Met Leu Val Ile Ser Leu Val Gly Met
 130 135 140
 Gly Ser Ala Thr Val Leu Met Gly Leu Leu Pro Gly Tyr Ala Gln Ile
 145 150 155
 Gly Ile Ala Ala Pro Ile Leu Leu Thr Leu Leu Arg Leu Val Gln Gly
 160 165 170 175
 Phe Ala Val Gly Gly Glu Trp Gly Gly Ala Thr Leu Met Ala Val Glu
 180 185 190
 His Ala Pro Thr Ala Lys Lys Gly Phe Phe Gly Ser Phe Ser Gln Met
 195 200 205
 Gly Ala Pro Ala Gly Thr Ser Val Ala Thr Leu Ala Phe Phe Ala Val
 210 215 220
 Ser Gln Leu Pro Asp Glu Gln Phe Leu Ser Trp Gly Trp Arg Leu Pro
 225 230 235
 Phe Leu Phe Ser Ala Val Leu Ile Val Ile Gly Leu Phe Ile Arg Leu
 240 245 250 255
 Ser Leu Ala Glu Ser Pro Asp Phe Ala Glu Val Lys Ala Gln Ser Ala
 260 265 270
 Val Val Arg Met Pro Ile Ala Glu Ala Phe Arg Lys His Trp Lys Glu
 275 280 285
 Ile Leu Leu Ile Ala Gly Thr Tyr Leu Ser Gln Gly Val Phe Ala Tyr
 290 295 300
 Ile Cys Met Ala Tyr Leu Val Ser Tyr Gly Thr Thr Val Ala Gly Ile
 305 310 315
 Ser Arg Thr Phe Ala Leu Ala Gly Val Phe Val Ala Gly Ile Val Ala
 320 325 330 335
 Val Leu Leu Tyr Leu Val Phe Gly Ala Leu Ser Asp Thr Phe Gly Arg
 340 345 350
 Lys Thr Met Tyr Leu Leu Gly Ala Ala Ala Met Gly Val Val Ile Ala
 355 360 365
 Pro Ala Phe Ala Leu Ile Asn Thr Gly Asn Pro Trp Leu Phe Met Ala
 370 375 380
 Ala Gln Val Leu Val Phe Gly Ile Ala Met Ala Pro Ala Ala Gly Val
 385 390 395
 Thr Gly Ser Leu Phe Thr Met Val Phe Asp Ala Asp Val Arg Tyr Ser
 400 405 410 415
 Gly Val Ser Ile Gly Tyr Thr Ile Ser Gln Val Ala Gly Ser Ala Phe
 420 425 430
 Ala Pro Thr Ile Ala Thr Ala Leu Tyr Ala Ser Thr Asn Thr Ser Asn
 435 440 445
 Ser Ile Val Thr Tyr Leu Leu Ile Val Ser Ala Ile Ser Ile Val Ser
 450 455 460
 Val Ile Leu Leu Pro Gly Gly Trp Gly Arg Lys Gly Ala Ala Ser Gln
 465 470 475
 Leu Thr Arg Asp Gln Ala Thr Ser Thr Pro Lys Met Pro Asp Thr Glu
 480 485 490 495
 Thr Phe Ser Thr Arg Thr Val Pro Asp Thr Ala Ala Ser Leu Arg Val
 500 505 510

Leu Asp Lys
515

<210> 4
<211> 638
<212> PRT
<213> Rhodococcus sp.

<400> 4

Val Met Thr Asp Met Ser Asp His Asp Arg Thr Ser Tyr Asp Thr
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Asp Val Val Ile Val Gly Leu Gly Pro Ala Gly Gly Thr Ala Ala Leu
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Ala Leu Ala Ser Tyr Gly Ile Arg Val His Ala Val Ser Met Phe Pro
35 40 45
Trp Val Ala Asn Ser Pro Arg Ala His Ile Thr Asn Gln Arg Ala Val
50 55 60
Glu Val Leu Arg Asp Leu Gly Val Glu Asp Glu Ala Arg Asn Tyr Ala
65 70 75
Thr Pro Trp Asp Gln Met Gly Asp Thr Leu Phe Thr Thr Ser Leu Ala
80 85 90 95
Gly Glu Glu Ile Val Arg Met Gln Thr Trp Gly Thr Gly Asp Ile Arg
100 105 110
Tyr Gly Asp Tyr Leu Ser Gly Ser Pro Cys Thr Met Leu Asp Ile Pro
115 120 125
Gln Pro Leu Met Glu Pro Val Leu Ile Lys Asn Ala Ala Glu Arg Gly
130 135 140
Ala Val Ile Ser Phe Asn Thr Glu Tyr Leu Asp His Ala Gln Asp Glu
145 150 155
Asp Gly Val Thr Val Arg Phe Arg Asp Val Arg Ser Gly Thr Val Phe
160 165 170 175
Thr Gln Arg Ala Arg Phe Leu Leu Gly Phe Asp Gly Ala Arg Ser Lys
180 185 190
Ile Ala Glu Gln Ile Gly Leu Pro Phe Glu Gly Glu Leu Ala Arg Ala
195 200 205
Gly Thr Ala Tyr Ile Leu Phe Asn Ala Asp Leu Ser Lys Tyr Val Ala
210 215 220
His Arg Pro Ser Ile Leu His Trp Ile Val Asn Ser Lys Ala Gly Phe
225 230 235
Gly Glu Ile Gly Met Gly Leu Leu Arg Ala Ile Arg Pro Trp Asp Gln
240 245 250 255
Trp Ile Ala Gly Trp Gly Phe Asp Met Ala Asn Gly Glu Pro Asp Val
260 265 270
Ser Asp Asp Val Val Leu Glu Gln Ile Arg Thr Leu Val Gly Asp Pro
275 280 285
His Leu Asp Val Glu Ile Val Ser Arg Ser Phe Trp Tyr Val Asn Arg
290 295 300
Gln Trp Ala Glu His Tyr Gln Ser Gly Arg Val Phe Cys Gly Gly Asp
305 310 315
Ala Val His Arg His Pro Pro Ser Ser Gly Leu Gly Ser Asn Thr Ser
320 325 330 335
Met Gln Asp Ala Phe Asn Leu Ala Trp Lys Ile Ala Phe Val Val Lys
340 345 350
Gly Tyr Ala Gly Pro Gly Leu Leu Glu Ser Tyr Ser Pro Glu Arg Val
355 360 365

Pro Val Gly Lys Gln Ile Val Ala Arg Ala Asn Gln Ser Arg Lys Asp
 370 375 380
 Tyr Ala Gly Leu Arg Glu Trp Phe Asp His Glu Ser Asp Asp Pro Val
 385 390 395
 Ala Ala Gly Leu Ala Lys Leu Lys Glu Pro Ser Ser Glu Gly Val Ala
 400 405 410 415
 Leu Arg Glu Arg Leu Tyr Glu Ala Leu Glu Val Lys Asn Ala Glu Phe
 420 425 430
 Asn Ala Gln Gly Val Glu Leu Asn Gln Arg Tyr Thr Ser Ser Ala Val
 435 440 445
 Val Pro Asp Pro Glu Ala Gly Glu Glu Val Trp Val Arg Asp Arg Glu
 450 455 460
 Leu Tyr Leu Gln Ala Thr Thr Arg Pro Gly Ala Lys Leu Pro His Ala
 465 470 475
 Trp Leu Val Gly Ala Asp Gly Thr Arg Ile Ser Thr Leu Asp Val Thr
 480 485 490 495
 Gly Lys Gly Met Met Thr Leu Leu Thr Gly Leu Gly Gly Gln Ala Trp
 500 505 510
 Lys Arg Ala Ala Lys Leu Asp Leu Pro Phe Leu Arg Thr Val Val
 515 520 525
 Val Gly Glu Pro Gly Thr Ile Asp Pro Tyr Gly Tyr Trp Arg Arg Val
 530 535 540
 Arg Asp Ile Asp Glu Ala Gly Ala Leu Leu Val Arg Pro Asp Gly Tyr
 545 550 555
 Val Ala Trp Arg His Ser Ala Pro Val Trp Asp Asp Thr Glu Ala Leu
 560 565 570 575
 Thr Ser Leu Glu Asn Ala Leu Thr Ala Val Leu Asp His Ser Ala Ser
 580 585 590
 Asp Asn Gly Asn Pro Ser Gly Thr Asn Glu Pro Gln Tyr Ser Thr Arg
 595 600 605
 Ala Val Pro Ile Val Val Pro His Val Thr Ala Glu Asp Ala Ala Pro
 610 615 620
 Ala Ser Ala Thr Arg Thr Thr Val Glu Gly Glu Asn Arg
 625 630 635

<210> 5
 <211> 315
 <212> PRT
 <213> Rhodococcus sp.

<400> 5
 Met Pro Val Ala Leu Cys Ala Met Ser His Ser Pro Leu Met Gly
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 Arg Asn Asp Pro Glu Gln Glu Val Ile Asp Ala Val Asp Ala Ala Phe
 20 25 30
 Asp His Ala Arg Arg Phe Val Ala Asp Phe Ala Pro Asp Leu Ile Val
 35 40 45
 Ile Phe Ala Pro Asp His Tyr Asn Gly Val Phe Tyr Asp Leu Leu Pro
 50 55 60
 Pro Phe Cys Ile Gly Ala Ala Ala Gln Ser Val Gly Asp Tyr Gly Thr
 65 70 75
 Glu Ala Gly Pro Leu Asp Val Asp Arg Asp Ala Ala Tyr Ala Val Ala
 80 85 90 95
 Arg Asp Val Leu Asp Ser Gly Ile Asp Val Ala Phe Ser Glu Arg Met
 100 105 110
 His Val Asp His Gly Phe Ala Gln Ala Leu Gln Leu Leu Val Gly Ser
 115 120 125

Ile Thr Ala Val Pro Thr Val Pro Ile Phe Ile Asn Ser Val Ala Glu
 130 135 140
 Pro Leu Gly Pro Val Ser Arg Val Arg Leu Leu Gly Glu Ala Val Gly
 145 150 155
 Arg Ala Ala Ala Lys Leu Asp Lys Arg Val Leu Phe Val Gly Ser Gly
 160 165 170 175
 Gly Leu Ser His Asp Pro Pro Val Pro Gln Phe Ala Thr Ala Pro Glu
 180 185 190
 Glu Val Arg Glu Arg Leu Ile Asp Gly Arg Asn Pro Ser Ala Ala Glu
 195 200 205
 Arg Asp Ala Arg Glu Gln Arg Val Ile Thr Ala Gly Arg Asp Phe Ala
 210 215 220
 Ala Gly Thr Ala Ala Ile Gln Pro Leu Asn Pro Glu Trp Asp Arg His
 225 230 235
 Leu Leu Asp Val Leu Ala Ser Gly Asp Leu Glu Gln Ile Asp Ala Trp
 240 245 250 255
 Thr Asn Asp Trp Phe Val Glu Gln Ala Gly His Ser Ser His Glu Val
 260 265 270
 Arg Thr Trp Ile Ala Ala Tyr Ala Ala Met Ser Ala Ala Gly Lys Tyr
 275 280 285
 Arg Val Thr Ser Thr Phe Tyr Arg Glu Ile His Glu Trp Ile Ala Gly
 290 295 300
 Phe Gly Ile Thr Thr Ala Val Ala Val Asp Glu
 305 310 315

<210> 6
 <211> 7599
 <212> DNA
 <213> Rhodococcus sp.

<220>
 <221> CDS
 <222> (4717)..(5586)
 <223> ohpC hydrolase

<400> 000

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	Met Thr Arg Pro Tyr Thr	
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agc gtc tgg gac gac ctg aac cag gtc gag ttc agc cag gga ttc atc		4782
Ser Val Trp Asp Asp Leu Asn Gln Val Glu Phe Ser Gln Gly Phe Ile		
10 15 20		
cag gcc ggc ccc tac cgg acc cga tac ctg cac gcc ggc gat tcg tcc		4830
Gln Ala Gly Pro Tyr Arg Thr Arg Tyr Leu His Ala Gly Asp Ser Ser		
25 30 35		
aag ccc acg ctg atc ctg ctg cac ggc atc acc ggc cac gcc gag gcg		4878
Lys Pro Thr Leu Ile Leu Leu His Gly Ile Thr Gly His Ala Glu Ala		
40 45 50		

tac gtg cgc aat ctg cgc tcg cat tcc gag cac ttc aac gtc tgg gca	4926
Tyr Val Arg Asn Leu Arg Ser His Ser Glu His Phe Asn Val Trp Ala	
55 60 65 70	
atc gac ttc atc ggc cac ggc tat tcg acc aag ccc gac cac ccg ctc	4974
Ile Asp Phe Ile Gly His Gly Tyr Ser Thr Lys Pro Asp His Pro Leu	
75 80 85	
gag atc aag cac tac atc gac cac gtg ctg cag ttg ctg gac gcc atc	5022
Glu Ile Lys His Tyr Ile Asp His Val Leu Gln Leu Leu Asp Ala Ile	
90 95 100	
ggc gtc gag aag gcc tcg ttt tcc ggg gag tct ctc ggc ggt tgg gtc	5070
Gly Val Glu Lys Ala Ser Phe Ser Gly Glu Ser Leu Gly Gly Trp Val	
105 110 115	
acc gcc cag ttc gcg cac gac cat ccc gag aag gtc gac cgg atc gtg	5118
Thr Ala Gln Phe Ala His Asp His Pro Glu Lys Val Asp Arg Ile Val	
120 125 130	
ctc aac acc atg ggc ggc acc atg gcc aac cct cag gtg atg gaa cgt	5166
Leu Asn Thr Met Gly Gly Thr Met Ala Asn Pro Gln Val Met Glu Arg	
135 140 145 150	
ctc tat acc ctg tcg atg gaa gcg gcg aag gac ccg agc tgg gaa cgc	5214
Leu Tyr Thr Leu Ser Met Glu Ala Ala Lys Asp Pro Ser Trp Glu Arg	
155 160 165	
gtc aaa gca cgc ctc gaa tgg ctc atg gcc gac ccg acc atg gtc acc	5262
Val Lys Ala Arg Leu Glu Trp Leu Met Ala Asp Pro Thr Met Val Thr	
170 175 180	
gac gac ctg atc cgc acc cgc cag gcc atc ttc cag cag ccg gat tgg	5310
Asp Asp Leu Ile Arg Thr Arg Gln Ala Ile Phe Gln Gln Pro Asp Trp	
185 190 195	
ctc aag gcc tgc gag atg aac atg gca ctg cag gac ctc gaa acc cgc	5358
Leu Lys Ala Cys Glu Met Asn Met Ala Leu Gln Asp Leu Glu Thr Arg	
200 205 210	
aag cgg aac atg atc acc gac gcc act ctc aac ggc atc acg gtg ccc	5406
Lys Arg Asn Met Ile Thr Asp Ala Thr Leu Asn Gly Ile Thr Val Pro	
215 220 225 230	
gcg atg gtg ctg tgg acc acc aag gac ccc tcc ggt ccg gtc gac gaa	5454
Ala Met Val Leu Trp Thr Thr Lys Asp Pro Ser Gly Pro Val Asp Glu	
235 240 245	
gcc aag cgc atc gcc tcc cac atc ccg ggc gcc aag ctg gcc atc atg	5502
Ala Lys Arg Ile Ala Ser His Ile Pro Gly Ala Lys Leu Ala Ile Met	
250 255 260	
gag aac tgt ggc cac tgg ccc cag tac gag gac ccc gag acc ttc aac	5550
Glu Asn Cys Gly His Trp Pro Gln Tyr Glu Asp Pro Glu Thr Phe Asn	
265 270 275	

aag ctg cat ctg gac ttc ctc ctc ggt cgc agc tga
 Lys Leu His Leu Asp Phe Leu Leu Gly Arg Ser
 280 285 290

5596

<210> 7
 <211> 289
 <212> PRT
 <213> Rhodococcus sp.

<400> 7

Met	Thr	Arg	Pro	Tyr	Thr	Ser	Val	Trp	Asp	Asp	Leu	Asn	Gln	Val	Glu	1	5	10	15
Phe	Ser	Gln	Gly	Phe	Ile	Gln	Ala	Gly	Pro	Tyr	Arg	Thr	Arg	Tyr	Leu	20	25	30	
His	Ala	Gly	Asp	Ser	Ser	Lys	Pro	Thr	Leu	Ile	Leu	Leu	His	Gly	Ile	35	40	45	
Thr	Gly	His	Ala	Glu	Ala	Tyr	Val	Arg	Asn	Leu	Arg	Ser	His	Ser	Glu	50	55	60	
His	Phe	Asn	Val	Trp	Ala	Ile	Asp	Phe	Ile	Gly	His	Gly	Tyr	Ser	Thr	65	70	75	80
Lys	Pro	Asp	His	Pro	Leu	Glu	Ile	Lys	His	Tyr	Ile	Asp	His	Val	Leu	85	90	95	
Gln	Leu	Leu	Asp	Ala	Ile	Gly	Val	Glu	Lys	Ala	Ser	Phe	Ser	Gly	Glu	100	105	110	
Ser	Leu	Gly	Gly	Trp	Val	Thr	Ala	Gln	Phe	Ala	His	Asp	His	Pro	Glu	115	120	125	
Lys	Val	Asp	Arg	Ile	Val	Leu	Asn	Thr	Met	Gly	Gly	Thr	Met	Ala	Asn	130	135	140	
Pro	Gln	Val	Met	Glu	Arg	Leu	Tyr	Thr	Leu	Ser	Met	Glu	Ala	Ala	Lys	145	150	155	160
Asp	Pro	Ser	Trp	Glu	Arg	Val	Lys	Ala	Arg	Leu	Glu	Trp	Leu	Met	Ala	165	170	175	
Asp	Pro	Thr	Met	Val	Thr	Asp	Asp	Leu	Ile	Arg	Thr	Arg	Gln	Ala	Ile	180	185	190	
Phe	Gln	Gln	Pro	Asp	Trp	Leu	Lys	Ala	Cys	Glu	Met	Asn	Met	Ala	Leu	195	200	205	
Gln	Asp	Leu	Glu	Thr	Arg	Lys	Arg	Asn	Met	Ile	Thr	Asp	Ala	Thr	Leu	210	215	220	
Asn	Gly	Ile	Thr	Val	Pro	Ala	Met	Val	Leu	Trp	Thr	Thr	Lys	Asp	Pro	225	230	235	240
Ser	Gly	Pro	Val	Asp	Glu	Ala	Lys	Arg	Ile	Ala	Ser	His	Ile	Pro	Gly	245	250	255	
Ala	Lys	Leu	Ala	Ile	Met	Glu	Asn	Cys	Gly	His	Trp	Pro	Gln	Tyr	Glu	260	265	270	
Asp	Pro	Glu	Thr	Phe	Asn	Lys	Leu	His	Leu	Asp	Phe	Leu	Leu	Gly	Arg	275	280	285	
Ser																			

<210> 8
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial
 Sequence:OHPR3

 <400> 8
 atcgaattcg gatccatgac caccacc 27

 <210> 9
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial
 Sequence:OHPR4

 <400> 9
 atcgcggccg ctctagacta actgcagggc gccaaagctcg gcag 44

 <210> 10
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial
 Sequence:C11

 <400> 10
 atcgaattcg gatccacgag agag 24

 <210> 11
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial
 Sequence:C12

 <400> 11
 atccggccgc gctctagagt acgcaagct 29

 <210> 12
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial
 Sequence:opl

 <400> 12
 atcctcgaga ccccgatacc 20

<210> 13
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial
Sequence:op2

<400> 13
atcgctcgacc gctaccc

17

<210> 14
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial
Sequence:CaMVop2

<400> 14
tccactgacg taagggatga cgcacaatcc cactatcctt cgcaagaccc

50

<210> 15
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial
Sequence:CaMVop3

<400> 15
atgctagacg tctagttcag acgctactta tatagaggaa gggctcttgcg

50

<210> 16
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial
Sequence:CaMVop4

<400> 16
cgtctagcat tctagttgag gaagttcatt tcatttggag aggac

45

<210> 17
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial
Sequence:CaMVopF1

<400> 17

atcgatatct ccactgacgt aag

23

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial
Sequence:CaMVopR1

<400> 18

gatggatccg tcctctccaa atga

24

<210> 19

<211> 470

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimaeric
promoter

<400> 19

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acctcctcgg	attccattgc	ccagctatct	gtcacttcat	cgaaaggaca	gtagaaaagg	180
aagatggctt	ctacaaatgc	catcattgcg	ataaaggaaa	ggctatcggt	caagaatgcc	240
tctaccgaca	gtggtcccaa	agatgtaccc	ccaccacga	ggaacatcgt	ggaaaaagaa	300
gacgttccaa	ccacgtcttc	aaagcaagtg	gattgatgtg	atatctccac	tgacgtaagg	360
gatgacgcac	aatcccacta	tccttcgcaa	gacccttcct	ctatataagt	agcgtctgaa	420
ctagacgtct	agcattctag	ttgaggaagt	tcatttcatt	tggagaggac		470